AMENDMENTS TO THE SPECIFICATION

Please amend the Specification at page 8, line 32 in the following manner:

Figures 18A and 18B show[[s]] Table 2, "Selected Seed-Specific Genes."

Please amend the Specification at page 9, line 1 in the following manner:

Figures 19A, 19B, and 19C show[[s]] Table 3, "Primers for PCR Amplification of 12 Promoter Regions."

Please amend the Specification at page 68, line 21 to page 69, line 17 in the following manner:

The plasmids of 2715 selected cDNA clones were collected from data set I. The inserts of the cDNAs were amplified by PCR in a 96-well format using primer pairs specific for the vector ends (for inserts in pBluescript SK-: T7, 5"-GTAATACGACTCACTATAGGGC (SEQ ID NO: [[13]]55), and 5" extended M13 reverse, 5"-ACAGGAAACAGCTATGACCATG (SEQ 113 NO: [[14]]56); for inserts in pZipLoxl: M13 forward, 5"-CCCAGTCACGACGTTGTAAAACG (SEQ ID NO: [[15]] 57) and M13 reverse, 5 "-AGCGGATAACAATTTCACACAGG) (SEQ ID NO: [[16]]58). PCR reactions of 100 gL volume contained 0.4 gM of each primer, 0.2 gM of each desoxynucleotide, 10 mM Tris, 50 mM KC1, 3.0 mM MgC12, 3 U Taq DNA polymerase (Promega, Madison) and -10 ng plasmid template. The reactions were run on a Perkin Elmer 9700 Thermoblock using an amplification program of 3 min denaturation at 94 C, 5 precycles of 30 s at 94 C, 30 s at 64 C, 2 min at 72 C, followed by 30 cycles of 30 s at 94 C, 30 s at 60 C, 2 min at 72 C and terminated by 7 min extension at 72 C. The PCR products were precipitated by adding 200 gL ethanol (95%) and 10 gL sodium acetate (3M, pH 5.2) and centrifugation at 3200 g and 4 C for 60 min. After washing with 80% ethanol, the DNA was resuspended in 20 gL 3x SSC. The yield and purity of the PCR products was analyzed by agarose gel electrophoresis. PCR samples showing by agarose gel analysis concentrations less than 0.2 gg/gL and/or double bands were repeated. If possible, alternative clones from the cDNA clone collection were used to repeat the PCR experiments. To reduce the cross-contamination risk in the 96-well

format, failed PCRs were not removed from the sample set, and as a result the number of PCR samples for printing increased by approximately 20%.

Please amend the Specification at page 74, lines 19-28, in the following manner:

Control vectors contained a GUS expression vector with either a napin or phaseolin promoter. For example, the promoter region of the napin (napA) gene in Brassica napus was amplified by using a forward primer CG aagctt TCTTCATCGGTGATT (SEQ ID NO: [[17]]59) and reverse primer GGTCG gaattc GTGTATGTTTT (SEQ ID NO: [[18]]60). The PCR product was digested by Hind III and EcoR I, then inserted into SK+ vector and confirmed by sequencing. The napin promoter was cut by Hind III and BamH I and inserted into a GUS expression vector such that GUS is under control of the napin promoter region. In a similar fashion, a GUS expression vector under control of a phaseolin promoter region was constructed; the phaseolin promoter region is described in patent US 5,504,200.